# High Throughput Sequencing
# National Germplasm Resources Laboratory

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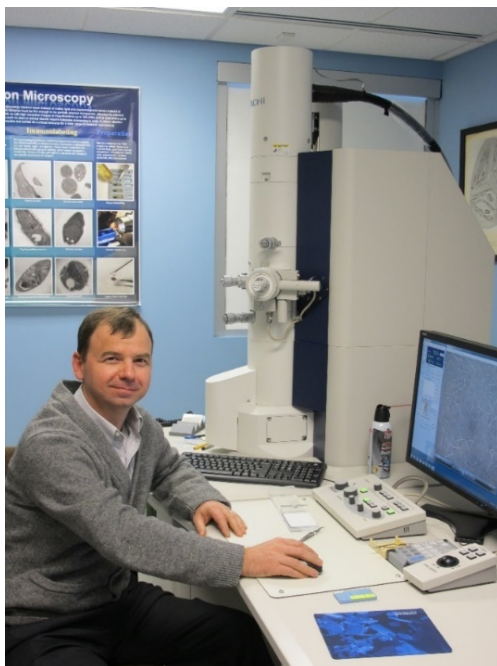
USDA

# National Germplasm Resources Lab

# Some NGS projects in my group
## Plant genera:

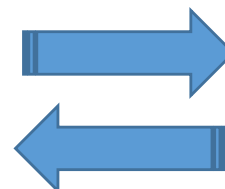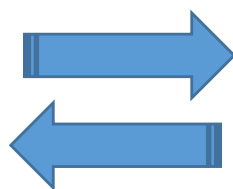| | | | |
|---|---|---|---|
| ***Saccharum*** | ***Solanum*** | *Rosa* | *Fraxinus* |
| *Sorghum* | | *Petunia* | *Rubus* |
| *Zea* | *Medicago* | *Syringa* | *Morus* |
| *Miscanthus* | *Nicotiana* | *Veronica* | *Ficus* |
| *Cynodon* | | *Iris* | *Carica* |
| *Lolium* | | *Lindera* | |
| *Stenotaphrum* | | | |
| *Rottboelia* | | | |
| *Panicum* | | | |
| *Phyllostachys* | | | |
| *Poa* | | | |
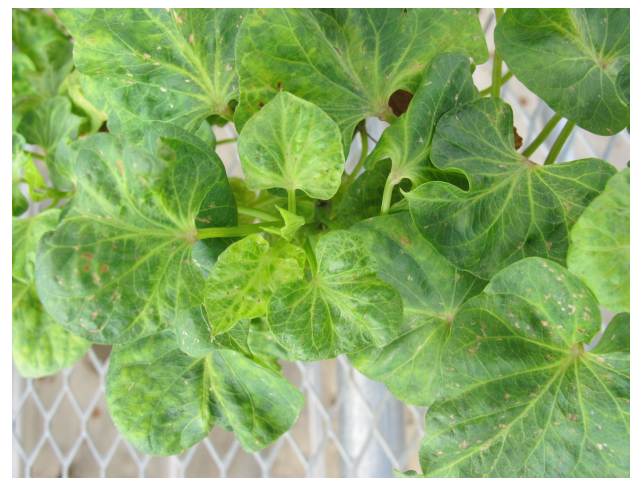
# PGQP – NGRL collaboration

Stakeholders        USDA APHIS        USDA ARS

PGQP: Plant Germplasm Quarantine Program
NGRL: National Resources Germplasm Laboratory

# HTS primary use in USDA programs*

- To evaluate shorter quarantine time
- To establish regulatory policy and permitting conditions
- To counter increased risks due to trade
- To develop policy regarding outcome of HTS
- To validate and establish HTS standards
- New virus discovery and characterization

*USDA APHIS -- USDA ARS

# HTS: Technological challenges

- **Developing efficient sample preparation methods for large scale application**

- **Developing bioinformatics algorithms to efficiently separate pathogen and host sequences**

# What is HTS positive sample?

**Questions:**

- How many total reads per sample?
- What is acceptable contig length?
- What is acceptable sequence depth?
- How many reads mapped into viral contig(s)?

# Factors to consider

- Total number of reads
- Percent sampled (subsample)
- Paired *vs.* single-ended reads
- Number of Contigs
- Reads Length
- Virus taxa
- Host
- Contig length
- Reads mapped
- Target sequence coverage depth

# *Saccharum spontaneum* accessions in Houma

MPTH97-461

MPTH98-388

# Thank you